

1	ATGCTGTTCCGCGCCCGGGGGCCGGTACGGGGCAGGGGCTGGGGGCGGCCGGCGCAGGCT	60
1	M L F R A R G P V R G R G W G R P A E A	20
61	CCCCCGCGGGGCGCTCGCCGCCCTGGAGCCCCGCCTGGATTGCTGCTGGGCGCTCGCC	120
21	P R R G R S P P W S P A W I C C W A L A	40
121	GGCTGCCAGGCGGCGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCGCGCCGCTTCCTCCT	180
41	G C Q A A W A G D L P S S S S R P L P P	60
181	TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG	240
61	C Q E K D Y H F E Y T E C D S S G S R W	80
241	AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC	300
81	R V A I P N S A V D C S G L P D P V R G	100
301	AAAGAATGCACTTTTCTCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC	360
101	K E C T F S C A S G E Y L E M K N Q V C	120
361	AGTAAGTGTGGTGAAGGCACCTATTCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT	420
121	S K C G E G T Y S L G S G I K F D E W D	140
421	GAATTGCCGGCAGGATTTTCTAACATCGCAACATTTCATGGACACTGTGGTGGGCCCTTCT	480
141	E L P A G F S N I A T F M D T V V G P S	160
481	GACAGCAGGCCAGACGGCTGTAACAACTCTTCTTGGATCCCTCGTGGAAGTACATAGAA	540
161	D S R P D G C N N S S W I P R G N Y I E	180
541	TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC	600
181	S N R D D C T V S L I Y A V H L K K S G	200
601	TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA	660
201	Y V F F E Y O Y V D N N I F F E F F I Q	220

661 AATGATCACTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACACACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

721 GGACAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260

781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280

841 ATTGAAGGGTGGCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTTCAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300

901 AAACCAGGTTCAATCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320

961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340

1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360

1081 AAGACACAGATAATGTACAAGTGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380

1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCCTGGATTT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400

1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420

1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B



FIG. 1C



1981	AACAATCAGGACCATTCGGTTTGCTATAGTGACTGCTTTTCTACCATGAAAAAGAAAAT	2040
661	N N Q D H S V C Y S D C F F Y H E K E N	680
2041	CAGATTTTGCACTATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC	2100
681	Q I L H Y D F S N L S S V G S L M N G P	700
2101	AGCTTCACCTCCAAAGGAACAAAATACTTCCATTCTTCAATATCAGTTTATGTGGGCAT	2160
701	S F T S K G T K Y F H F F N I S L C G H	720
2161	GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACACACTTTACAGTAAAAGAAATA	2220
721	E G K K M A L C T N N I T D F T V K E I	740
2221	GTGGCAGGGTCAGATGATTACACAAATTGGTAGGGCATTGTATGCCAGTCAACAATT	2280
741	V A G S D D Y T N L V G A F V C Q S T I	760
2281	ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA	2340
761	I P S E S K G F R A A L S S Q S I I L A	780
2341	GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAAGAAGAT	2400
781	D T F I G V T V E T T L K N I N I K E D	800
2401	ATGTTCCAGTTCCAACAAGCCAAATACCAGATGTGCATTTCTTTTATAAGTCTTCTACA	2460
801	M F P V P T S Q I P D V H F F Y K S S T	820
2461	GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT	2520
821	A T T S C I N G R S T A V K M R C N P T	840
2521	AAATCTGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG	2580
841	K S G A G V I S V P S K C P A G T C D G	860
2581	TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC	2640
861	C T F Y F L W E S A E A C P L C T E H D	880

FIG. 1D



FIG. 1E



FIG. 2A

	10	20	30								
1	MLFRARGFVRGRGWGRFAEAPRRGRSEFWS										TR16.aa
1	M	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
1	M	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	40	50	60								
31	PAWICCWALAGCQAAWAGDLSSSSRBLEPF										TR16.aa
10	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
13	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	70	80	90								
61	CQERDYHFEYTECDSSGSRWRVAIPNSAVD										TR16.aa
23	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
26	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	100	110	120								
91	CSGLPDEVRGKECTFSCASGEYLEMKNQVC										TR16.aa
30	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
31	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	130	140	150								
121	SKCGEGTYSLGSGIKFDEWDELPAQFSNIA										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	160	170	180								
151	TFMDTVVGPSDSRFDGCNNSSWIPIRGNYIE										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	190	200	210								
181	SNRDDCTVSLIYAVVELKKSGYVFFEYQYVD										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	220	230	240								
211	NNIFFEFFIIONDQCQEMDTTDDKWVKLTDN										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	250	260	270								
241	GEWGSHSVMLKSGTNILYWRTTGILMGSKA										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	280	290	300								
271	VKPVLVKNITIEGVAYTSECFPCPKPGTFSN										TR16.aa
51	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
	310	320	330								
301	KPGSFNCOVCPNNTYSEKGAKECIRCKDDS										TR16.aa
62	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
54	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40

FIG. 2B

	340	350	360	
331	Q F S G S S E C T E R E P E C T T R D Y F Q I H T E C D E E G			TR16.aa
66	-			EMB CAB41042.1 TNFR
58	-			emb CAA53576.1 OX40
	370	380	390	
361	K T Q I M Y K W I E P K I C R E D I T D A I R L P P S G E K			TR16.aa
66	-			EMB CAB41042.1 TNFR
58	-			emb CAA53576.1 OX40
	400	410	420	
391	K D C P P C N P G F Y N N G S S C H P C P P G T F S D G T			TR16.aa
70	T K C E R C P P H T Y T A I P N Y S N G C			EMB CAB41042.1 TNFR
62	T V C R P C G P G F Y N D V V S - S K P C			emb CAA53576.1 OX40
	430	440	450	
421	K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T			TR16.aa
91	H Q C R K C - - P T G S - - - - - F D K V			EMB CAB41042.1 TNFR
82	K P C T W C N L R S G S - - - - - E R K Q			emb CAA53576.1 OX40
	460	470	480	
451	S C F N V G N S K C D G M N G W E V A G D H I Q S G A G G S			TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S Q T - - - -			EMB CAB41042.1 TNFR
98	L C T A T Q D T V C R C R A G - - - - T Q P L D S - - - -			emb CAA53576.1 OX40
	490	500	510	
481	D N D Y L I L N L H I E G F K P E P T S M T G A T G S E L G R			TR16.aa
130	-			EMB CAB41042.1 TNFR
119	-			emb CAA53576.1 OX40
	520	530	540	
511	I T E V F E T L C S A D C V L Y F M V D I N R K S T N V V E			TR16.aa
132	-			EMB CAB41042.1 TNFR
122	-			emb CAA53576.1 OX40
	550	560	570	
541	S W G G T K E K Q A Y T H I I F K N A T F T F T W A F O R T			TR16.aa
137	-			EMB CAB41042.1 TNFR
127	-			emb CAA53576.1 OX40
	580	590	600	
571	N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S			TR16.aa
137	-			EMB CAB41042.1 TNFR
127	-			emb CAA53576.1 OX40
	610	620	630	
601	S C R A C A L G S E Q S G S S C V P C P P G H Y I E K E T N			TR16.aa
141	-			EMB CAB41042.1 TNFR
128	-			emb CAA53576.1 OX40

FIG. 2C

	640	650	660	
631	QCKRCPPDTYLSFHOVYGRKACIECGEGSK			TR16.aa
147	-----GGI			EMB CAB41042.1 TNFR
134	-----SPG			emb CAA53576.1 OX40
	670	680	690	
661	NNQDHSVCYSDCFEFYHKKENQILLHYDFSNI			TR16.aa
150	DEQGNPIC-----			EMB CAB41042.1 TNFR
137	DNCIA-----C			emb CAA53576.1 OX40
	700	710	720	
691	SSVGSILMNGESPFTSKGTRKFHFENISLCGH			TR16.aa
158	-----KSCV			EMB CAB41042.1 TNFR
142	-----KPWTNCTL			emb CAA53576.1 OX40
	730	740	750	
721	EGKRMALCTNNITDFTVKRIVAGSDDYTNL			TR16.aa
163	GE-----Y			EMB CAB41042.1 TNFR
150	AGKH-----TLQPASNSSDAI			emb CAA53576.1 OX40
	760	770	780	
751	VGAFVCOSTIIPSESKGFRAALSSQSILLA			TR16.aa
166	-----CD			EMB CAB41042.1 TNFR
166	-----CEDRDPPATQPQETQGP PARPTTVQ			emb CAA53576.1 OX40
	790	800	810	
781	DTFIGVTVETTLKNNIKEDMFPVPTSQIP			TR16.aa
168	-----			EMB CAB41042.1 TNFR
191	PT-----EAWPTTSQGP			emb CAA53576.1 OX40
	820	830	840	
811	DVHFFYKSSSTATTSCTINGRSTAVKMR CNPT			TR16.aa
168	-----			EMB CAB41042.1 TNFR
203	-----STRPVEVP GGR AVAAIL			emb CAA53576.1 OX40
	850	860	870	
841	KSGAGVISVPSKCEAGTCDGCTFYFLWESA			TR16.aa
168	-----			EMB CAB41042.1 TNFR
220	--GLGLV-----LGLL			emb CAA53576.1 OX40
	880	890	900	
871	EACPLCTEHDFFEIEGACKTGFOETLYVWN			TR16.aa
168	-----YLL			EMB CAB41042.1 TNFR
229	--GPL-----AILLA LYL L L R			emb CAA53576.1 OX40
	910	920	930	
901	EPRWCIGISLFEKKLATCETVDFWLKVA			TR16.aa
170	-----RNYRLDP			EMB CAB41042.1 TNFR
242	-----RDQRLEPDAHKP			emb CAA53576.1 OX40

940 950 960

931 **G V G A E T A V L L V A L T C E F W K K N Q K R K K T I L N** TR16.aa
177 - - - E - - - - - - - - - P P C K L S EMB CAB41042.1 TNFR
255 **G G G S E R T P I - - - - - Q E E Q A D A H S T L A** emb CAA53576.1 OX40

961	L F N	<input type="checkbox"/>
184	K C - N	
276	K I	

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TR16.aa
EMB | CAB41042.1 TNFR
emb | CAA53576.1 OX40

```

TR16.aa

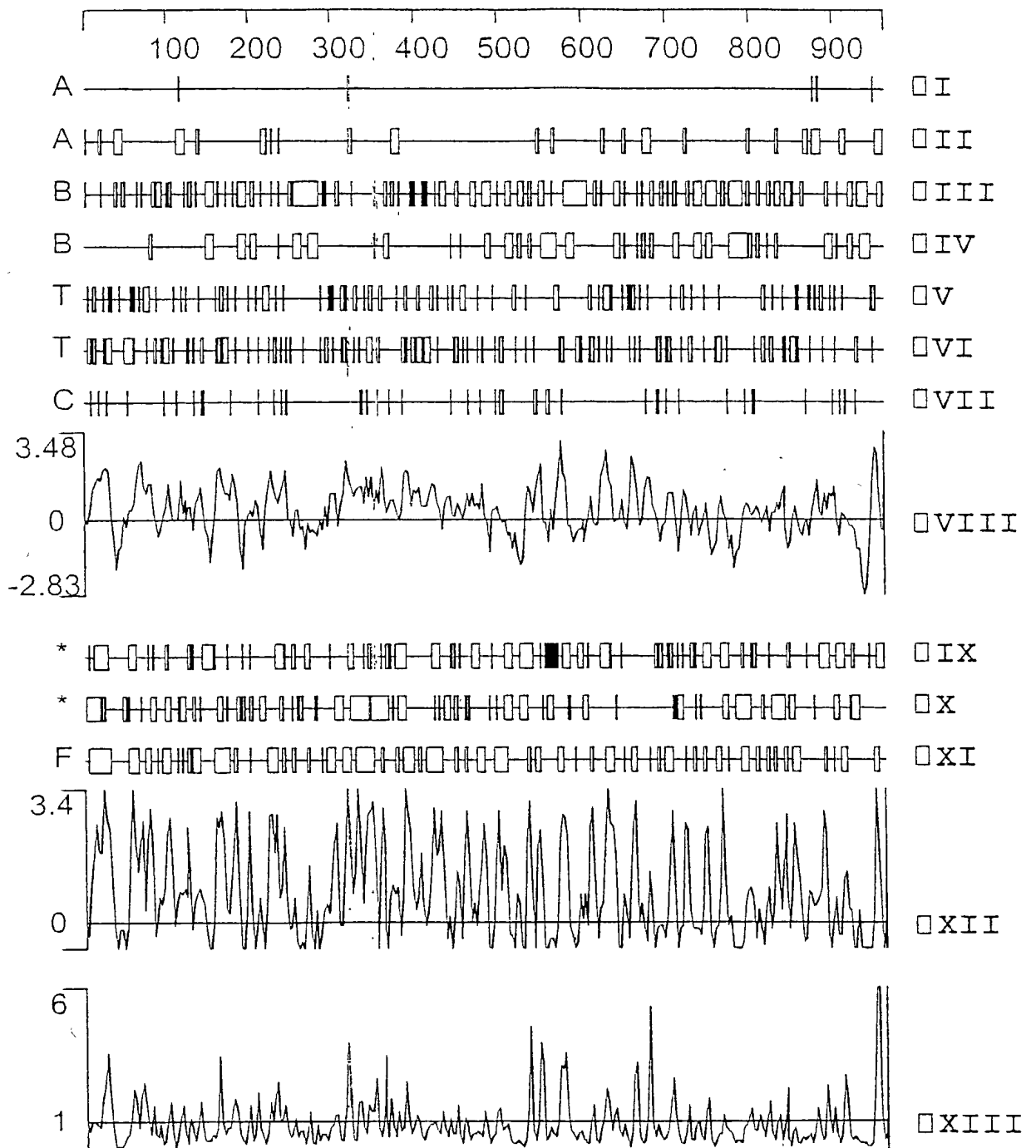


FIG. 3

FIG. 4A



721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
241 G E W G S H S V M L K S G T N I L Y W R 260

781 ACTACAGGCATCCTTATGGGTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
261 T T G I L M G S K A V K P V L V K N I T 280

841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAAC 900
281 I E G V A Y T S E C F P C K P G T F S N 300

901 AAACCAGGTTTCACTCAACTGCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960
301 K P G S F N C Q V C P R N T Y S E K G A 320

961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
321 K E C I R C K D D S Q F S G S S E C T E 340

1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
341 R P P C T T K D Y F Q I H T P C D E E G 360

1081 AAGACACAGATAATCTACAAGTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT 1140
361 K T Q I M Y K W I E P K I C R E D L T D 380

1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCCTGGATTT 1200
381 A I R L P P S G E K K D C P P C N P G F 400

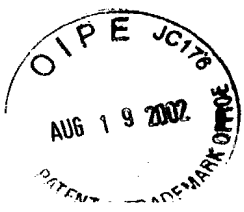
1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGGAACC 1260
401 Y N N G S S S C H P C P P G T F S D G T 420

1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
421 K E C R P C P A G T E P A L G F E Y K W 440

1321 TGGAAATGTCCTTCTGGAACATGAAACTTCCTGCTTCAATGTTGGGAATTCAAAGTGC 1380
441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGCTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B



1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTC A 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATCGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTCCGGTTCATCGTGTGCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGAAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGAAAGAGGCTTGTATTCCATCGGGGCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

1981 AACAAATCAGGACCATTGGGTTTGCTATAGTGAAGTCTTTTCTACCATGAAAAAGAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

2041 CAGATTTTGCATATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C



2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
721 E G K K M A L C T N N I T D F T V K E I 740

2221 GTGGCAGGGTCAGATGATTACACAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
741 V A G S D D Y T N L V G A F V C Q S T I 760

2281 ATTCCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
761 I P S E S K G F R A A L S S Q S I I L A 780

2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAAGAAGAT 2400
781 D T F I G V T V E T T L K N I N I K E D 800

2401 ATGTTCCAGTTCCAACAAGCCAAATACCAGATGTGCATTCTTTTATAAGTCTTCTACA 2460
801 M F P V P T S Q I P D V H F F Y K S S T 820

2461 GCAACAACATCTTGTATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
821 A T T S C I N G R S T A V K M R C N P T 840

2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGGCCAGCAGGTACCTGTGATGGG 2580
841 K S G A G V I S V P S K C P A G T C D G 860

2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
861 C T F Y F L W E S A E A C P L C T E H D 880

2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTTCAGGAAACCTTGATGTGTGGAAT 2700
881 F H E I E G A C K R G F Q E T L Y V W N 900

2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
901 E P K W C I K G I S L P E K K L A T C E 920

2761 ACCGTTGACTTTTGGCTGAAGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTTGCTG 2820
921 T V D F W L K V G A G V G A F T A V L L 940

2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAAGTGAATACAAATATTTCCAAG 2880
941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D



2881 TTAGTAATGACGACTAACTCAAAGAGTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
 961 L V M T T N S K E C E L P A A D S C A I 980

2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000
 981 M E G E D N E E E V V Y S N K Q S L L G 1000

3001 AAACTCAAATCTTTGGCAACCAAGGAAAAAGAAGACCATTTTGAATCTGTTCAACTGAAA 3060
 1001 K L K S L A T K E K E D H F E S V Q L K 1020

3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTGTGTAGCCTTGAGACTAATGAACAAA 3120
 1021 T S R S P N I * 1028

3121 GAAACCTGCTCTAGTTTACAGGACCATATTTTAGGGTCTGTCCTCATACCTGTGACATT 3180

3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGAAGGAGATTGAAACATTTGATT 3240

3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTGCGGTCTCAA 3300

3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360

3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACCTTTTATT 3420

3421 CTTTATGATGTCTACATAACAAGTGTGATTTGGAAGGCACATGTGAGCATATGCATTATG 3480

3481 ATCCAATTTATGTTTTTCTTTGTTTATATTTTGGGAAAATTAAATTTTTTTAAGGTA 3540

3541 AAAAAAAAAAAAAA 3556

FIG. 4E



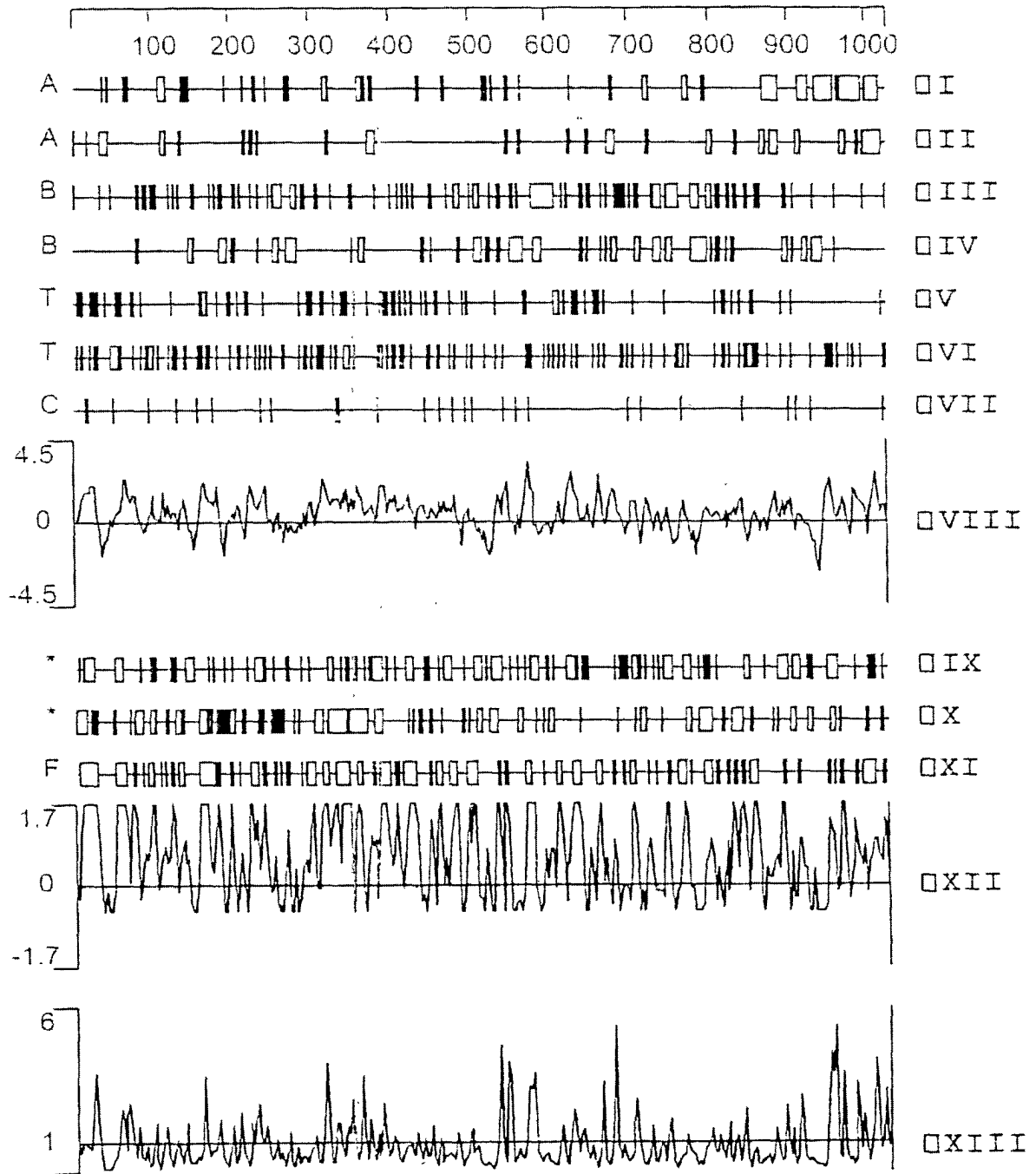


FIG. 5

	10	20	30	40	
1	M L F R A R G P V R G R G W G R P A E A P R R G R S P P W S P A W I C C W A L A				SEQ ID 2
1	-----				SEC10
	50	60	70	80	
41	G C Q A A W A G D L P S S S S R P L P P C Q E K D Y H F E Y T E C D S S G S R W				SEQ ID 2
1	-----				SEC10
	90	100	110	120	
81	R V A I P N S A V D C S G L P D P V R G K E C T F S C A S G E Y L E				SEQ ID 2
1	-----				SEC10
	130	140	150	160	
121	S K C G E G T Y S L G S G I R E D E W D E L P A G F S N I A T F M D T V V G P S				SEQ ID 2
7	S K C G E G T Y S L G S G I R E D E W D E L P A G F S N I A T F M D T V V G P S				SEC10
	170	180	190	200	
161	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEQ ID 2
47	D S R P D G C N N S S W I P R G N Y I E S N R D D C T V S L I Y A V H L K K S G				SEC10
	210	220	230	240	
201	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D R K W V K L T D N				SEQ ID 2
37	Y V F F E Y Q Y V D N N I F F E F F I Q N D Q C Q E M D T T T D R K W V K L T D N				SEC10
	250	260	270	280	
241	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V R P V L V K N I T				SEQ ID 2
127	G E W G S H S V M L K S G T N I L Y W R T T G I L M G S K A V R P V L V K N I T				SEC10
	290	300	310	320	
281	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E R G A				SEQ ID 2
167	I E G V A Y T S E C F P C K P G T F S N K P G S F N C Q V C P R N T Y S E R G A				SEC10
	330	340	350	360	
321	K E C I R C K D D S Q F S - - G S S E C T E R P P C T T K D Y F Q I H T P C D E				SEQ ID 2
207	K E C I R C K D D S Q F S E E G S S E C T E R P P C T T K D Y F Q I H T P C D E				SEC10
	370	380	390	400	
359	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P S G E R K D C P P C N P				SEQ ID 2
247	E G K T Q I M Y K W I E P K I C R E D L T D A I R L P S G E R K D C P P C N P				SEC10
	410	420	430	440	
399	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEQ ID 2
287	G F Y N N G S S S C H P C P P G T F S D G T K E C R P C P A G T E P A L G F E Y				SEC10
	450	460	470	480	
439	K W W N V L P G N M R T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEQ ID 2
327	K W W N V L P G N M R T S C F N V G N S K C D G M N G W E V A G D H I Q S G A G				SEC10
	490	500	510	520	
479	G S D N D Y L I L N L H I P G G K P P T S M T G A T G S E L G R I T F V F E T L				SEQ ID 2
267	G S D N D Y L I L N L H I P G G K P P T S M T G A T G S E L G R I T F V F E T L				SEC10

FIG. 6A



519	CSADCVLYFMVDINRRKSTNVVSWGGTKRKQAYTHLIPRN	SEQ ID 2		
407	CSADCVLYFMVDINRRKSTNVVSWGGTKRKQAYTHLIPRN	SEC10		
530	540	550	560	
559	ATPTFTWAFQR	TNNQGQDNRRFINDMVKIYSITATNAVDGV	SEQ ID 2	
447	ATPTFTW	GIPIRE	SEC10	
610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD	SEQ ID 2		
459			SEC10	
650	660	670	680	
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVQYSDCFFYHEK	SEQ ID 2		
459			SEC10	
690	700	710	720	
679	ENQILHYDFSNLSSVGS	LMNGB	SFTSKGTKYFHFNFNLSLC	SEQ ID 2
459		LIQGER		SEC10
730	740	750	760	
719	GREGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFFVCQS	SEQ ID 2		
464			SEC10	
770	780	790	800	
759	TIIPSESKGFRAALSSQSIIILADTFIGVTVETTLKNINIK	SEQ ID 2		
464			SEC10	
810	820	830	840	
799	EDMFPVPPTSQIPDVHFFFYKSSSTATTS	CINGRSTAVKMR	SEQ ID 2	
464			SEC10	
850	860	870	880	
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE	SEQ ID 2		
464			SEC10	
890	900	910	920	
879	HDFHEIEGACKRGRGFQETLYVWNEPKWC	IKGISLPEKKLAT	SEQ ID 2	
464			SEC10	
930	940	950	960	
919	CETVDFWLKVGAGVGAF	TAVLLVALTCYFWKKNQKKKKTI	SEQ ID 2	
464			SEC10	
959	LNLFN	SEQ ID 2		
464		SEC10		

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

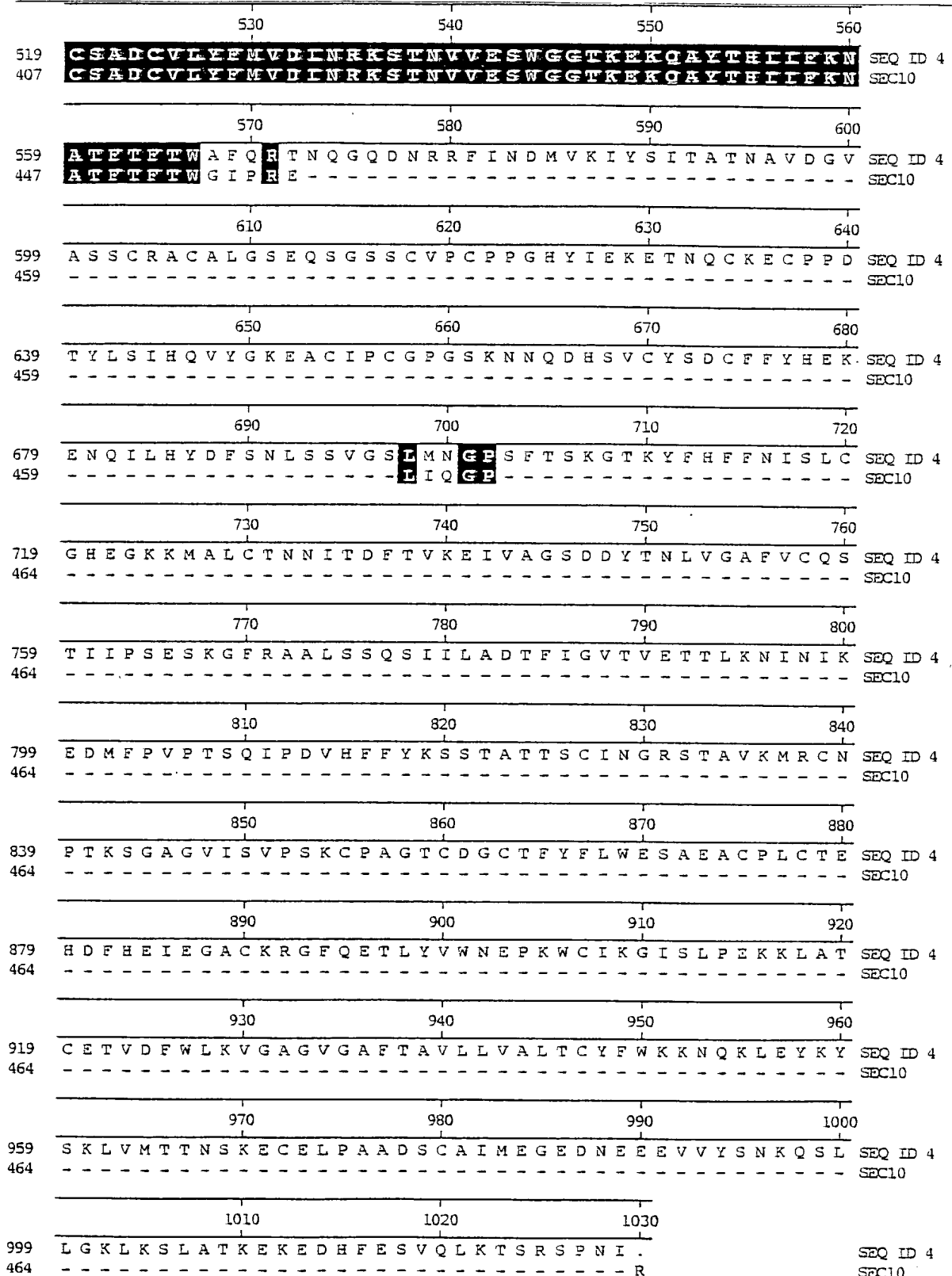
FIG. 6B



	10	20	30	40	
1	MLTRARGPVRGRGWGRPAZAPRRGRSPSPWSPAWICCWALIA				SEQ ID 4
1	-----				SEC10
	50	60	70	80	
41	GCQAAWAGDLPSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 4
1	-----				SEC10
	90	100	110	120	
81	RVAIPNSAVDCCSGLPDPVRGKECTFS CAGGEYLE				SEQ ID 4
1	-----				SEC10
	130	140	150	160	
121	SKCGEGTYSLSGSGIKFDEWDELPA GFSNIATFMDTVVGPS				SEQ ID 4
7	SKCGEGTYSLSGSGIKFDEWDELPA GFSNIATFMDTVVGPS				SEC10
	170	180	190	200	
161	DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKS				SEQ ID 4
47	DSRPDGCNNSSWIPRGNYIESNRDDCTVSLIYAVHLKKS				SEC10
	210	220	230	240	
201	YVFEFYQYVDNNIEFFFIQNDQCQEMD TTTDRWVKLTDN				SEQ ID 4
37	YVFEFYQYVDNNIEFFFIQNDQCQEMD TTTDRWVKLTDN				SEC10
	250	260	270	280	
241	GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEQ ID 4
127	GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEC10
	290	300	310	320	
281	IEGVAYTSECFPCRPCTFSNKP GSFNCQVCPRNTYSEKGA				SEQ ID 4
167	IEGVAYTSECFPCRPCTFSNKP GSFNCQVCPRNTYSEKGA				SEC10
	330	340	350	360	
321	KECIRCKDDSQES -- GSSECTERPPCTTKDYFOIHTPCDE				SEQ ID 4
207	KECIRCKDDSQFSE E GSSECTERPPCTTKDYFOIHTPCDE				SEC10
	370	380	390	400	
359	EGKTQIMYRWIEPKICREDLTD ARLPPSGEKKDCPPCNP				SEQ ID 4
247	EGKTQIMYRWIEPKICREDLTD ARLPPSGEKKDCPPCNP				SEC10
	410	420	430	440	
399	GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFY				SEQ ID 4
287	GFYNNGSSSCHPCPPGTFS DGTKECRPCPAGTEPALGFY				SEC10
	450	460	470	480	
439	KWWNVLEGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEQ ID 4
327	KWWNVLEGNMKTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEC10
	490	500	510	520	
479	GSDNDYLLILNLHIEGPKPPTSMTGATGSELGRITFVPEETL				SEQ ID 4
367	GSDNDYLLILNLHIEGPKPPTSMTGATGSELGRITFVPEETL				SEC10

FIG. 7A





Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B

